This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

1. (currently amended) A collection of lines of transgenic animals comprising two or more of said lines of transgenic animals wherein each of said transgenic animals comprises a transgene, said transgene comprising (a) first sequences coding for a selectable or detectable marker protein; and (b) regulatory sequences of a characterizing gene corresponding to an endogenous gene or ortholog of an endogenous gene operably linked to said first sequences such that said first sequences are expressed in said transgenic animal with an expression pattern that is substantially the same as the expression pattern of said endogenous gene in a non-transgenic animal or anatomical region thereof, wherein the characterizing gene is different for each of said transgenic animals, wherein said first sequences are not expressed in said transgenic animals prior to the animals being made transgenic, and wherein said transgene is present in the genome at a site other than where the endogenous gene is located.

2. (Original) The collection of lines of transgenic animals of claim 1 wherein said transgenic animals are transgenic mice.

3. (Original) The collection of lines of transgenic animals of claim 1 which comprises ten or more lines of transgenic animals.

4. (Original) The collection of lines of transgenic animals of claim 1 which comprises fifty or more lines of transgenic animals.

5. (Original) The collection of lines of transgenic animals of claim 1 wherein said transgene further comprises a coding sequence of said characterizing gene.

6. (Original) The collection of lines of transgenic animals of claim 5 wherein said first sequences are inserted or replace sequences 5' of said coding sequence of said characterizing gene.

7. (currently amended) The collection of lines of transgenic animals of claim 1 wherein said first sequences are operably linked to an IRES sequence ~~that is not operably linked to a coding sequence of said characterizing gene~~.

8. (Original) The collection of lines of transgenic animals of claim 5 wherein said first sequences are fused in frame to the ATG start codon of said coding sequence of said characterizing gene.

9. (Original) The collection of lines of transgenic animals of claim 1 wherein said characterizing gene is not functionally expressed from said transgene.

10. (Original) The collection of lines of transgenic animals of claim 1 wherein said first sequences encode a detectable enzyme.

11. (Original) The collection of lines of transgenic animals of claim 10 wherein said detectable enzyme is β-lactamase.

12. (Original) The collection of lines of transgenic animals of claim 1 wherein said first sequences encode a fluorescent protein.

13. (Original) The collection of lines of transgenic animals of claim 12 wherein fluorescent protein is a green fluorescent protein (GFP).

14. (Original) The collection of lines of transgenic animals of claim 1 wherein each said endogenous gene is expressed in the same tissue.

15. (Original) The collection of lines of transgenic animals of claim 1 wherein each said endogenous gene is specifically expressed in a subset of neurons.

16. (Original) The collection of lines of transgenic animals of claim 1 wherein each said endogenous gene is endogenously expressed in neuronal cells.

17. (Original) The collection of lines of transgenic animals of claim 1 wherein each of said endogenous genes endogenously expresses a protein product that is a part of an adrenergic or noradrenergic neurotransmitter pathway, a cholinergic neurotransmitter pathway, a dopaminergic neurotransmitter pathway, a GABAergic neurotransmitter pathway, a glutaminergic neurotransmitter pathway, a glycinergic neurotransmitter pathway, a histaminergic neurotransmitter pathway, a neuropeptidergic neurotransmitter pathway, a serotonergic neurotransmitter pathway, or the sonic hedgehog signaling pathway, is a nucleotide receptor, an ion channel, a marker of undifferentiated or not fully differentiated nerve cells, a calcium binding protein, or a neurotrophic factor receptor.

18. (Original) The collection of lines of transgenic animals of claim 1 wherein all of said endogenous genes are functionally related.

19. (Original) The collection of lines of transgenic animals of claim 1 wherein each of said endogenous genes is implicated in the same physiological or disease state.

20. (Original) The collection of lines of transgenic animals of claim 19 wherein the physiological or disease state is a neurological or psychiatric disease.

21. (Original) The collection of lines of transgenic animals of claim 20 wherein the neurological or psychiatric disease is schizophrenia, schizotypal personality disorder, psychosis, a schizoaffective disorder manic type disorder, a bipolar affective disorder, a bipolar affective (mood) disorder with hypomania and major depression (BP-II), a unipolar affective disorder, unipolar major depressive disorder, dysthymic disorder, a obsessive-compulsive disorder, a phobia, a panic disorder, a generalized anxiety disorder, a somatization disorder, hypochondriasis, or an attention deficit disorder.

22. (Original) The collection of lines of transgenic animals of claim 1 wherein each of said endogenous genes is implicated in the same physiological or behavioral response.

23. (Original) The collection of lines of transgenic animals of claim 22 wherein said physiological or behavioral response is pain, sleeping, feeding, fasting, sexual behavior or aggression.

24. (Original) The collection of lines of transgenic animals of claim 1 wherein each of said endogenous genes is expressed in neuronal cells involved in regulation of feeding behavior.

25. (Original) The collection of lines of transgenic animals of claim 1 wherein each of said endogenous genes is expressed in a different tissue.

26. (Original) The collection of lines of transgenic animals of claim 1 wherein each of said endogenous genes is implicated in a different physiological or disease state.

27. (Original) The collection of lines of transgenic animals of claim 1 wherein each of said endogenous genes is implicated in a different physiological or behavioral response.

28-31. (Canceled)

32. (Original) A method of making a collection of lines of transgenic animals said method comprising

(a) introducing into the genome of a founder animal a transgene comprising (i) first sequences coding for a selectable or detectable marker protein and (ii) regulatory sequences of a characterizing gene corresponding to an endogenous gene or ortholog of an endogenous gene operably linked to said first sequences such that said first sequences are expressed in said transgenic animal with an expression pattern that is substantially the same as the expression pattern of said endogenous gene in a non-transgenic animal or anatomical region thereof and said first sequences are not expressed in said transgenic animals prior to the animals being made transgenic,;

(b) breeding said founder animal to produce a line of transgenic animals; and

(c) repeating steps (a) and (b) one or more times, each time with a different characterizing gene to generate one or more additional lines of transgenic animals,

thereby generating said collection of lines of transgenic animals.

33. (Original) The method of claim 32 wherein said transgenic animals are transgenic mice.

34. (Original) The method of claim 32 wherein said collection comprises ten or more lines of transgenic animals.

35. (Original) The method of claim 32 wherein said collection comprises fifty or more lines of transgenic animals.

36. (Original) The method of claim 32 wherein said transgene further comprises a coding sequence of said characterizing gene.

37. (Original) The method of claim 36 wherein said first sequences are inserted or replace sequences 5' of said coding sequence of said characterizing gene.

38. (currently amended) The method of claim 32 wherein said first sequences are operably linked to an IRES sequence ~~that is not operably linked to a coding sequence of said characterizing gene~~.

39. (Original) The method of claim 36 wherein said first sequences are fused in frame to the ATG start codon of said coding sequence of said characterizing gene.

40. (Original) The method of claim 32 wherein said characterizing gene is not functionally expressed from said transgene.

41. (Original) The method of claim 32 wherein said first sequences encode a detectable enzyme.

42. (Original) The method of claim 41 wherein said detectable enzyme is β-lactamase.

43. (Original) The method of claim 32 wherein said first sequences encode a fluorescent protein.

44. (Original) The method of claim 43 wherein fluorescent protein is a GFP.

45. (Original) The method of claim 32 wherein each said endogenous gene is expressed in the same tissue.

46. (Original) The method of claim 32 wherein each said endogenous gene is specifically expressed in a subset of neurons.

47. (Original) The method of claim 32 wherein each said endogenous gene is endogenously expressed in neuronal cells.

48. (Original) The method of claim 32 wherein each of said endogenous genes endogenously expresses a protein product that is a part of an adrenergic or noradrenergic neurotransmitter pathway, a cholinergic neurotransmitter pathway, a dopaminergic neurotransmitter pathway, a GABAergic neurotransmitter pathway, a glutaminergic neurotransmitter pathway, a glycinergic neurotransmitter pathway, a histaminergic neurotransmitter pathway, a neuropeptidergic neurotransmitter pathway, a serotonergic neurotransmitter pathway, or the sonic hedgehog signaling pathway, is a nucleotide receptor, an ion channel, a marker of undifferentiated or not fully differentiated nerve cells, a calcium binding protein, or a neurotrophic factor receptor.

49. (Original) The method of claim 32 wherein all of said endogenous genes are functionally related.

50. (Original) The method of claim 32 wherein each of said endogenous genes is implicated in the same physiological or disease state.

51. (Original) The method of claim 50 wherein the physiological or disease state is a neurological or psychiatric disease.

52. (Original) The method of claim 51 wherein the neurological or psychiatric disease is schizophrenia, schizotypal personality disorder, psychosis, a schizoaffective disorder manic type disorder, a bipolar affective disorder, a bipolar affective (mood) disorder with hypomania and major depression (BP-II), a unipolar affective disorder, unipolar major depressive disorder, dysthymic disorder, a obsessive-compulsive disorder, a phobia, a panic disorder, a generalized anxiety disorder, a somatization disorder, hypochondriasis, or an attention deficit disorder.

53. (Original) The method of claim 32 wherein each of said endogenous genes is implicated in the same physiological or behavioral response.

54. (Original) The method of claim 53 wherein said physiological or behavioral response is pain, sleeping, feeding, fasting, sexual behavior or aggression.

55. (Original) The method of claim 32 wherein each of said endogenous genes is expressed in neuronal cells involved in regulation of feeding behavior.

56. (Original) The method of claim 32 wherein each of said endogenous genes is expressed in a different tissue.

57. (Original) The method of claim 32 wherein each of said endogenous genes is implicated in a different physiological or disease state.

58. (Original) The method of claim 32 wherein each of said endogenous genes is implicated in a different physiological or behavioral response.

59. (Original) The method of claim 32 wherein prior to introduction into said founder animal said transgene is contained within a bacterial artificial chromosome (BAC).

60. (Original) The method of claim 32 wherein said transgene is introduced by pronuclear injection.

61-158. (Canceled)